

Figure 1:

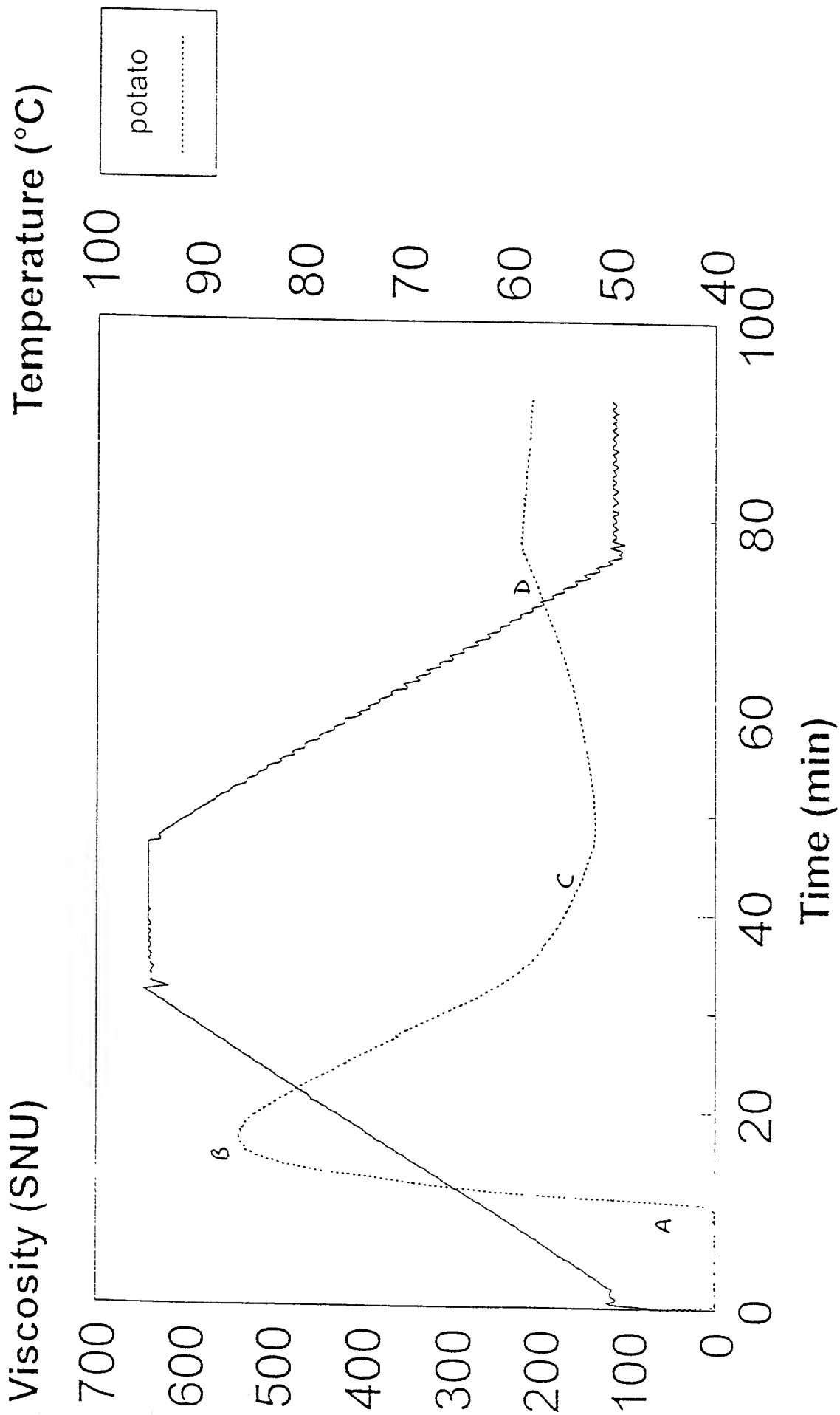
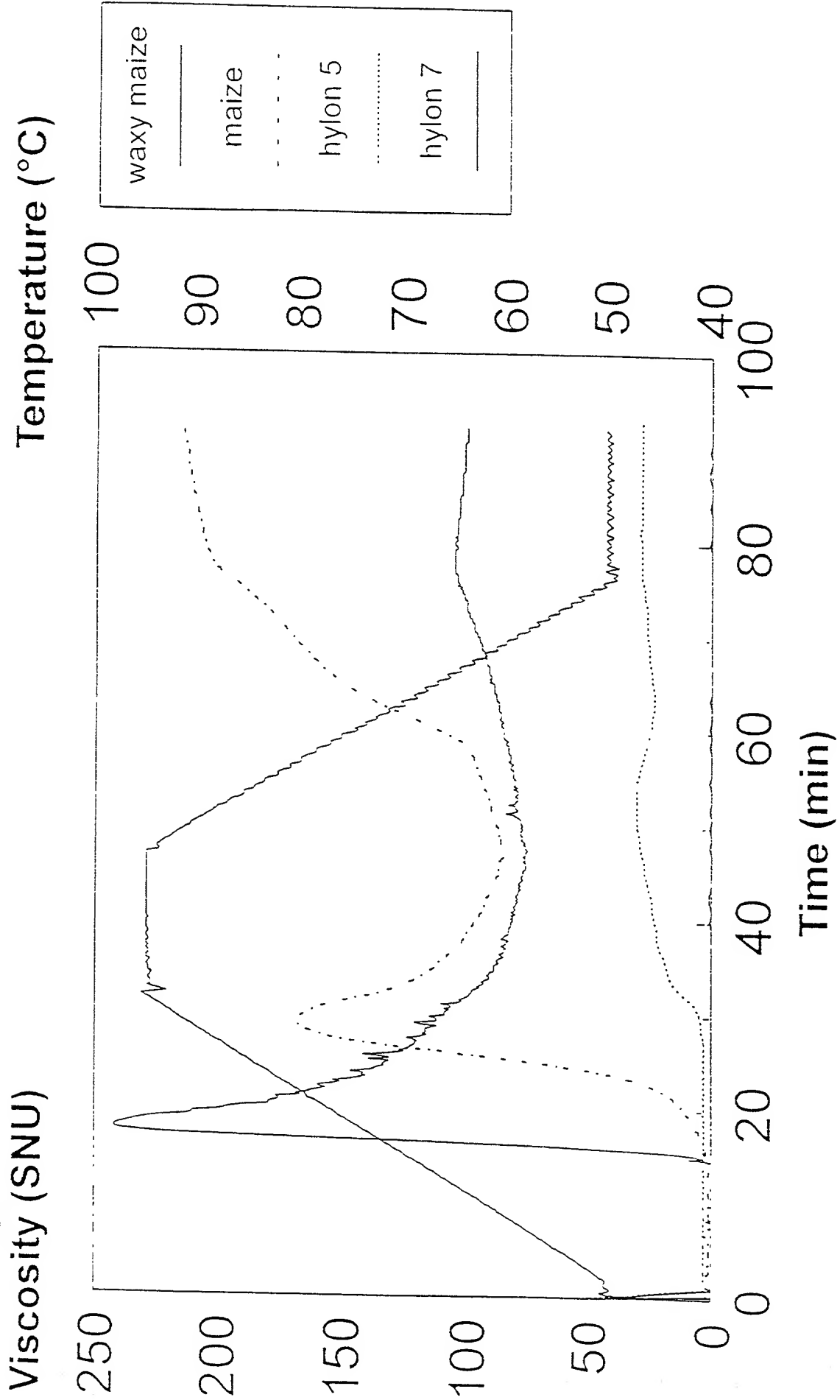


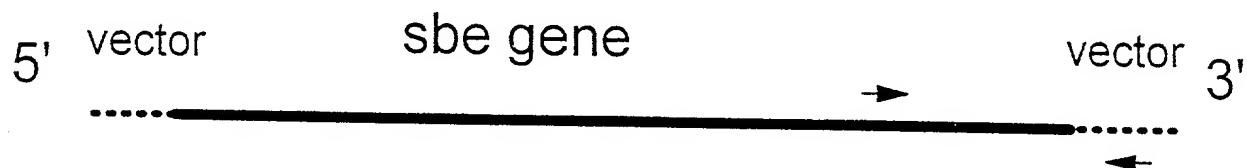
Figure 2:



NH₂

COOH

protein alignment
design primer



PCR library

850 bp

screen library

1200 bp

1500 bp

RACE

190 bp

150 bp

450 bp

750 bp

1400 bp

204370-149500T

204310"454500T

Fig. 4a

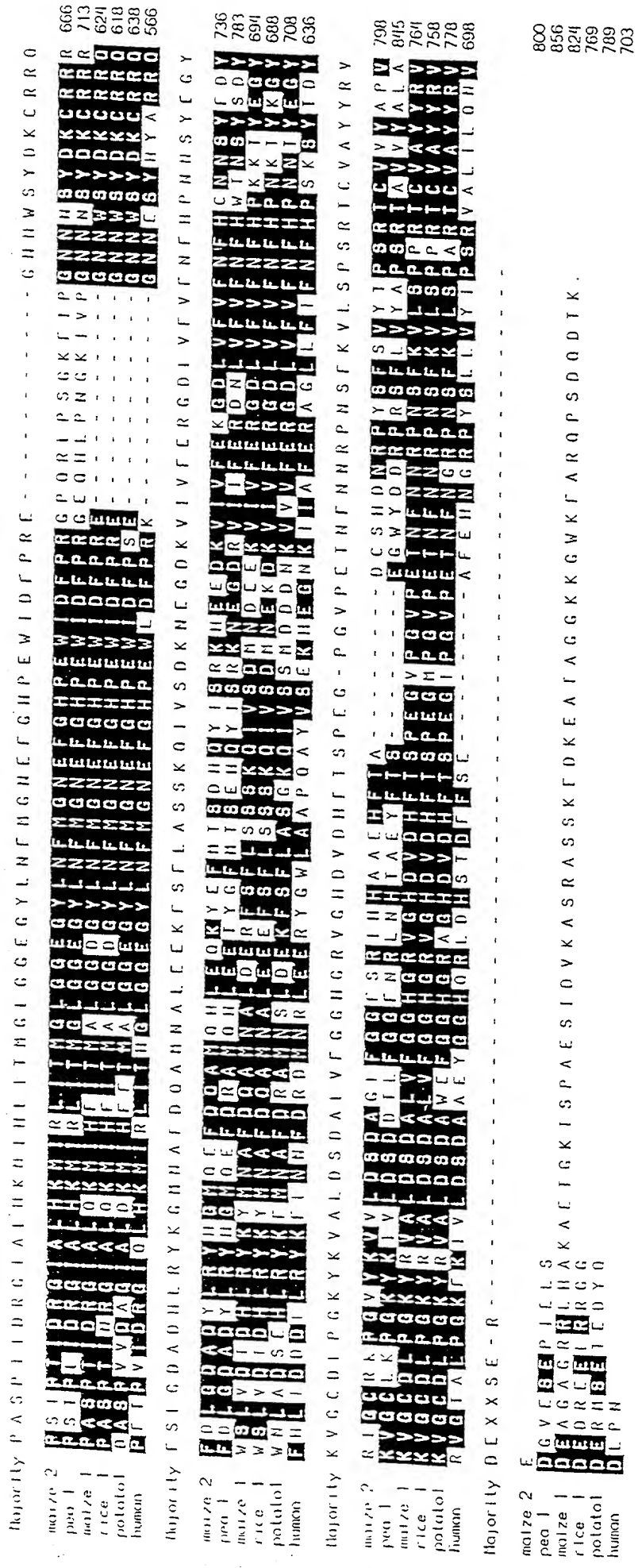
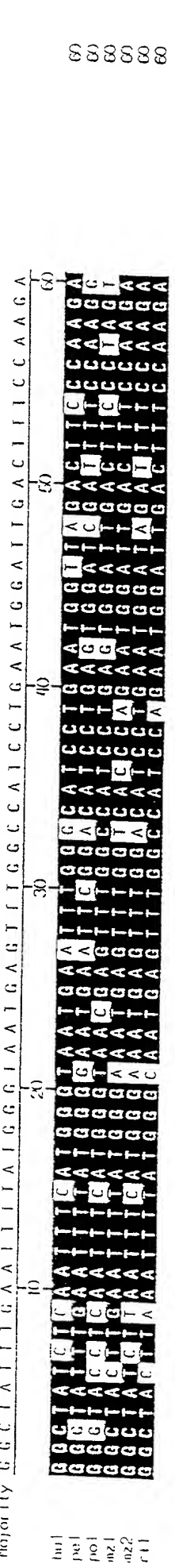


Fig. 4b



CAGCTTCCTGATGAAATTCATATAATGGAATACATTATGATCCACCCGAAGAGGAGGATATCTTCCAACACCCACGGCCAAAGAAA
 GTCGAAGGACTACTTTAAGGTATATTACCTTATGTAATACTAGGTGGGCTTCTCCTCTCCATATAGAAGGTTGTGGGTGCCGGTTCTTT
 O L P D E I P Y N G I H Y D P P E E E R Y I F Q H P R P K K

Xmn I

CCAAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAAATTAACTCATACGTGAATTTAGAGATGAAGTT
 GGTTCAGCGACTCTTATATACTTAGAGTATAACCTTACTCATCAGGCCTCGGATTTTAATTGAGTATGCACTTAAAACTCTCTACTTCAA
 P K S L R I Y E S H I G M S S P E P K I N S Y V N F R D E V

HinD III

CTTCCTCGCATAAAAAAGCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTACGCTAGTTTGGTTATCATGTC
 GAAGGAGCGTATTTTTTCGAACCCATGTTACGCGACGCTTAAATACCGATAAGTTCTCGTAAGAATAATGCGATCAAAACCAATAGTACAG
 L P R I K K L G Y N A L O I M A I Q E H S Y Y A S F G Y H V

ACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACGCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTT
 TGTTTAAAAAACGTTGTTCTGTCGGCAAAACCTTTCGGGCTGCTGGAATTCAGAACTAACTATTTGAGTACTCGATCCTTAACAACAA
 T N F F A P S S R F G T P D D L K S L I D K A H E L G I V V

CTCATGGACATTGTTTACAGCCATGCATCAAATAATACTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTTTCACCTCT
 GAGTACCTGTAACAAGTGTGCGGTACGTAGTTTATTATGAAATCTACCTGACTTGTACAAACTGACGTGGCTATCAACAATGAAAGTGAGA
 L M D I V H S H A S N N T L D G L N M F O C T D S C Y F H S

Sac I

GGAGCTCGTGGTTATCATTGGATGTGGGATTCCTCGCTCTTTAACTATGGAACCTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGA
 CCTCGAGCACCATAAGTAACCTACACCTAAGGGCGGAGAAATTGATACCTTTGACCTCCATGAATCCATAGAAGAGAGTTTACGCTCT
 G A R G Y H W M W D S R L F N Y G N W E V L R Y L L S N A R

TGGTGGTTGGATGCGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACCACGGATTATCGGTGGGATTC
 ACCACCAACCTACGCAAGTTTAACTACCTAAATCTAACTACCACACTGTAGTTACTACATATAAGTGGTGCCTAATAGCCACCTAAG
 W W L D A F K F D G F R F D G V T S M M Y I H H G L S V G F

Hinc II

ACTGGGAACACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTT
 TGACCTTGATGCTCCTTATGAAACCTGAGCGTTGACTACACCTACGACAACACATAGACTACGACCACTTCTAGATAAAGTACCCGAA
 T G N Y E E Y F G L A T D V D A V V Y L M L V N D L I H G L

TTCCAGATGCAATTACCATTTGGTGAAGATGTTAGCGGAATGCCGACATTTTGATTCCCGTCCAAGAGGGGGGTGTTGGCTTTGACTAT
 AAGGGTCTACGTTAATGGTAACCACTTCTACAATCGCTTACGGCTGTAAACATAAAGGGCAGGTTCTCCCCCACAACCGAAACTGATA
 F P D A I T I G E D V S G M P T F C I P V C E G G V G F D Y

CGGCATGATGGCAATGCTGATAAACGGATGAGTTGCTCAAGAAACGGGATGAGGAATGGAGAGGGGATGATTTGTTCAACACG
 GCGGACATACCGTTAACGACATTTTGGCTAACTCAACGAGTTCTTTGCCCCACTCCTAACCTCTCACCACATATAACAAGTATGTGAC
 P L - M A I A D K P I E L L K K R D E D W P V G D I V H T L

ACAAATAGAAGATGGTCGAAAAGTGTTTCAACGCTGAAAGTCATGATCAAGCTCTAGTCGCTGATAAACTATAGCATTTCTGGCTG
 TTTTATCTTCTACGAGCTTTTACACAAAAGTATGCGACTTTCAGTACTAGTTTCGAGATCAGCCACTATTTTGAATCGTAAGACCGAC
 T N R P W S E K C V S Y A E S - D G A L V G D K T I A F W L

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ATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAAATAGATCGTGGGATAGCATTGCACAAGATGATTAGG
TACCTGTTCTTATACATACTAAAATACCGAGACCTATCTGGCAGTTGTAGTAATTATCTAGCACCCCTATCGTAACGTGTTCTACTAATCC
M D K D M Y D F M A L D R P S T S L I D R G I A L H K M I R 2160

EcoRI

CTTGTAACTATGGGATTAGGAGGAGAAGGGTACCTAAATTTTCATGGGAAATGAATTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCT
2250
GAACATTGATACCTAATCTCTCTCTCCCATGGATTTAAAGTACCCTTTACTTAAGCCGGTGGGACTCACCTAACTAAAGGGATCCCGA
L V T M G L G G E G Y L N F M G N E F G H P E W I D F P R A

GAACAACACCTCTCTGATGGCTCAGTAATCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTGACCTGGGAGATGCAGAA
CTTGTGTGGAGAGACTACCGAGTCATTAGGGGCCCTTTGGTTAAGTCAATACTATTACGTCCTGCCTCTAAACTGGACCTCTACGCTT
E Q H L S D G S V I P G N Q F S Y D K C R R R F D L G D A E 2340

TATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGCCTATGCAGTATCTTGAAGATAAAATAGAGTTTATGACTTCAGAACACCAAGTTC
ATAAATTTCTATGGCACCCAACGTTCTTAAACTGGCCGGATACGTCATAGAAGTCTTATTTATACTCAAATACTGAAGTCTTGTGGTCAAG
Y L R Y R G L Q E E D R P M O Y L E D K Y E F M T S E H Q F 2430

ATATCACGAAAGGATGAAGGAGATAGGATGATTGTAATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTAT
TATAGTGCTTTCTACTTCCTCTATCCTACTAACAATAAACTTTTTCTTTGGATCAAAAAACAGAAATTTAAAGTGACCTGTTTTTCGATA
I S R K D E G D R M I V F E K G N L V F V F N F H W T K S Y 2520

TCAGACTATCGCATAGCCTGCCTGAAGCCTGGAAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAATT
AGTCTGATAGCGTATCGGACGGACTTCGGACCTTTTATGTTCCAACGGAACCTGAGTCTACTAGGTGAAAAACCACCGAAGCCCTCTTAA
S D Y R I A C L K P G X Y K V A L D S D D P L F G G F G R I

GATCATAATGCCGAATATTTACCTTTGAAGGATGGTATGATGATCGTCTCGTTCAATTATGGTGTATGCACCTTGTA AACACAGCAGTG
CTAGTATTACGGCTTATAAAGTGGAAACTTCTACCATACTACTAGCAGGAGCAAGTTAATACCACATACGTGGAACATTTTGTGTCAC 2700
D H N A E Y E I F E G W Y D D R P R S I M V Y A P C K T A V

[illegible]

TGAACGAACCTTGATCCCGTTAAAGATTGGAACGCTACATAGAGCTTCTTGACGTATCTGGCAATATTGCATCAGTCTTGGCGGAAT 2880
ACTTGCTTGAACACTAGCGCAACTTTCTAAACTTGCATGTATCTCGAAGAACTGCATAGACGGTTATAACGTAGTCAGAACCGGCTTAA

TCA TGTAC TCACAGG TTTGCAT TTTGCAT ATAG TAG GCATCGAT TACGCAGAGT GAAG GC GAACAACT ATG AAAATC
 2970
 AGTACAGT ATGTTCCCAACAG TTAGCAAGG GATATTCATCAGG TGC ATATGCGTCTCTACTTCAGGACTGTTGTATACATTTTAG

GATGAATTAACTCGAATGCTGGGACGATCGAATCCTGCAGGCGGGGGACCCCTTAGTTC
CTACTTAAATACAGCTTACGATCCCTGCTAGCTTAAAGGACGTCGGGGCCCCCTGGGGAATCAAGA 3033

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✓180 ✓190 ✓200 ✓210 ✓220
IYEIDPLLTNYRQHLDYRYSQYKKLREAIDKYEGGLEAFSRGYEKMGFTR
: : : DP L. Y : H: . R . : Y . : I: KYEG LE. F: : GY K. GF. R
LLNLDPTLEPYLDHFRHRMKRYVDQKMLIEKYEGPLEEFAQGYLKFGFN
^100 ^110 ^120 ^130 ^140
✓230 ✓240 ✓250 ✓260 ✓270
SATGITYREWALGAQSAALIGDFNNWDANADIMTRNEFGVWEIFLPNNVD
... I. YREWA : AQ. A. : IGDFN. W: : : : M. : : : FGVW. I : P: VD
EDGCIVYREWAPAAQEA E VIGDFNGWNGSNHMMEKDQFGVWSIRIPD-VD
^150 ^160 ^170 ^180 ^190
✓280 ✓290 ✓300 ✓310 ✓320
GSPAIPHGSRVKIRMDTPSGV-KDSIPAWINYSLOLPDEI--PYNGIHYD
: . P. IPH. SRVK: R. . : GV D. IPAWI: Y: . : : : PY: G: . . D
SKPVIPHNSRVKFRFKHNGVWVDRIPAWIKYATADATKFAAPYDGVYWD
^200 ^210 ^220 ^230 ^240
✓330 ✓340 ✓350 ✓360 ✓370
PPEEERYIFQHPRPKPKSLRIYESHIGMSSPEPKINSYVNFRRDEVLPRI
PP . ERY F: . PRP KP: : RIYE: H: GMSS: EP: : NSY : F D: VLPRI
PPPSERYHFKYPRPPKPRAPRIYEAHVGMSSSEPRVNSYREFADDVLPRI
^250 ^260 ^270 ^280 ^290
✓380 ✓390 ✓400 ✓410 ✓420
KKLGYNALQIMAIQEHSSYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAH
K . YN: : Q: MAI EHSYY: SFGYHVTNFFA S: R: G. P: DLK LIDKAH
KANNYNTVOLMAIMEHSYYGSFGYHVTNFFAVSNRYGNPEDLKYLIDKAH
^300 ^310 ^320 ^330 ^340
✓430 ✓440 ✓450 ✓460 ✓470
ELGIVVLMDIVHSHASNNTLDGLNMFDC---TDSCYFHSGARGYHWMWDS
. LG: VL: D: VHSHASN. DGLN FD : : : YFH: G. RGYH : WDS
SLGLQVLVDVHSHASNNVTDGLNGFDIGQGSQESYFHAGERGYHKLWDS
^350 ^360 ^370 ^380 ^390
✓480 ✓490 ✓500 ✓510 ✓520
RLFNYGNWEVLRYL LSNARWWLDAFKFDGFRFDGVTSMYIHHGLSVGFT
RLFNY: NWEVLR: LLSN RWWL: . : : FDGFRFDG: TSM: Y: HHG: : : GFT
RLFNYANWEVLRFL LSNLRWWLEENFDGFRFDGITSMLYVHHGINMGFT
^400 ^410 ^420 ^430 ^440
✓530 ✓540 ✓550 ✓560 ✓570
GNYEEYFGLATDVDVAVVYLMVNDLIHGLFPDAITIGEDVSGMPTFCIPV
GNY: EYF: ATDVDVAVVYLM. N: LIH : FPDA. . I: EDVSGMP: . PV
GNYNEYFSEATDVDVAVVYLMANL!HKIFPDATVIAEDVSGMPGLSRPV
^450 ^460 ^470 ^480 ^490
✓580 ✓590 ✓600 ✓610 ✓620
QEGGVGFDYRLHMAIADKRIELLK-KRDEDWRVGDIVHTLTNRWSEKCV
EGG: GFDYRL MAI: DK: I: LK K. DEGW : : : : LTNR : EKC:
SEGGIGFDYRLMAIPCKWIDYLNKNDEEDWSMKEVTSSLTNRRYTEKCI
^500 ^510 ^520 ^530 ^540

F.g. 6

8/31

10056454.012402

SYAESHQQALVGDKTIAFWLMDKDMYDFMALDRPSTSLIDRGIALHKMIR
: YAESHQQ: : VGDKTIAF LMDK: MY. M: : : : : DRGIALHKMI:
AYAESHQQSIVGDKTIAFL LMDKEMYSGMSCLTDASPVVDRGIALHKMIH
^550 ^560 ^570 ^580 ^590
LVTMGLGGEGYLNFMGNEFGHPEWIDFPRAEQHLSOGSVIPGNQFSYDKC
: TM: LGGEGYLNFMGNEFGHPEWIDFPR GN: . SYDKC
FFTALGGEGYLNFMGNEFGHPEWIDFPR-----EGNNWSYDKC
^600 ^610 ^620 ^630
RRRFDLGDAEYLR YRGLQEFDRPMQYLEDKYEFMTSEHQFISRKDEGDRM
RR: . : L: D: E. LRY: . : . FDR: M: L: : K: . F: : S. . Q: : S. . D: : : :
RRQWNLADSEHLRYKFMNAFDRAMNSLDEKFSFLASGKQIVSSMDDDNKV
^640 ^650 ^660 ^670 ^680
IVFEKGNLVFVFNFWTKSYSDYRIACLKPGKYKVALDSDDPLFGGFGRI
: VFE: G: LVFVFNFH . : . Y. : Y: : : C PGKY: VAL: SD. FGG GR
VVFERGDLVFVFNFHNPNTYEGYKVGCDLPGKYRVALGSDAWFEGGHGRA
^690 ^700 ^710 ^720 ^730
DHNAEYFT-----FEGWYDDRPRSIMVYAPCKTAVVYALVDKEEEEE
: H: . : . FT E. : : : RP. S: . V : P : T V. Y VD. . E.
GHDVDHFTSPEGIPGVPETNFNGRPNSFKVLSPARTCVAYYRVDERMSET
^740 ^750 ^760 ^770 ^780
EEEEEEV
E: . : . :
EDYQTDI
^790

Fig. 6 (con.)

10056454-012402

↖10 ↖20 ↖30 ↖40
MVYTL SGVRFP TVPSVYK SNGFSSNGDRRNANVSVFLKKH--SLSRKILA
MVYT: SG: RFP: PS: KS : . DRR.: S FLK.: S: SR. L
MVYTL SGIRFPVLP SLHKS---TLRCDRRASSHSFFLKNNSSSF SRTSLY
^10 ^20 ^30 ^40
↖50 ↖60 ↖70 ↖80 ↖90
EKSSYNSEFRPSTVAASGKVLVPGTOSDSSSSSTQFEFTETSPENSPAS
.K S : SE : ST: A. S: KVL: P. Q D: S S : DQ: E . . . : E: . .
AKFSRDSETKSSTIAESDKVLIPEDQ-DNSVSLADQLENPDITSEDAQNL
^50 ^60 ^70 ^80 ^90
↖100 ↖110 ↖120 ↖130 ↖140
TDVDSSTMEHASQ!KTENDDVEPSSDLTGSVEELODFASSLQLQEGGKLEE
.D: TM.: . . . : . . . : . . . : S : . . . : .
EDL---TMKDGKNKYNI D-ESTSSYREV GDEKGSVTSSSLVDVNTDTQ--A
^100 ^110 ^120 ^130 ^140
↖150 ↖160 ↖170 ↖180 ↖190
SKTLNTSEETI IDESDRIRERGIPPPGLGQKIYEIDPLL TNYRQHLDYRY
.KT S: . . . : . : I IPPPG GQKIYEIDPLL . RQHLD: RY
KKT SVHSDKKVKVDKPKI----IPPPGSGQKIYEIDPLLQAH RQHLD FRY
^150 ^160 ^170 ^180
↖200 ↖210 ↖220 ↖230 ↖240
SQYKKLREAI DKYEGGLEAFSRGYEKM GFTRSATGITYREWALGAQSAAL
: QYK: : RE. IDKYEGGL: AFSRGYEK. GFTRSATGITYREW: GA: SAAL
GOYKRIREE IDKYEGGLDAFSRGYEKF GFTRSATGITYREWGP GAKSAAL
^190 ^200 ^210 ^220 ^230
↖250 ↖260 ↖270 ↖280 ↖290
IGDFNNDANADIMTRNEFGVWEIFLPNNVDGSPAIPHGSRVKIRMDTPS
: GDFNNW: : NAD: MT: . . FGVWEIFLPNN. DGSP: IPHGSRVKI: MDTPS
VGDFNWNPNADVMTKDAFGVWEIFLPNNADGSPPIPHGSRVKIHMDTPS
^240 ^250 ^260 ^270 ^280
↖300 ↖310 ↖320 ↖330 ↖340
GVKDSIPAWINYSLQLPDEIPYNGIHYDPPEEERYIFCHPRPKPKSLRI
G: KDSIPAWI: : S: Q P: EIPYNGI. YOPPEE: Y: F: HP: PK: P: S: RI
GIKDSIPAWIKFSVQAPGEIPYNGIYYDPPEE EK YVFKHPQPKRPOSIRI
^290 ^300 ^310 ^320 ^330
↖350 ↖360 ↖370 ↖380 ↖390
YESHIGMSSPEPKINSYVNF RDEVLPRIKKLGYNALCIMA IQEHSYYASF
YESHIGMSSPEPKIN: Y. NFRD: VLPRIKKLGYN: QIMAIQEHSYYASF
YESHIGMSSPEPKINTYANFRDVLPR IKKLGYNVQIMAIQEHSYYASF
^340 ^350 ^360 ^370 ^380
↖400 ↖410 ↖420 ↖430 ↖440
GY-VTNFFAPSSRFGT PDDLKSL:DKAHELGI VVLMCIVHSHASNNTLDG
GY-VTNFFAPSSRFGT: DLKSLID: AHELGI: VVLMCIVHSH: SNNTLDG
GY-VTNFFAPSSRFGT PEDLKSL: DRAHELGLLVLMCIVHSHSSNNTLDG
^390 ^400 ^410 ^420 ^430

Fig 7

10/31

10056454-012402

↖450 ↖460 ↖470 ↖480 ↖490
LNMFDCTDSCYFHSRGARGYHWMWDSRLFNNGWVLRYL LSNARWWLDAF
LNMFD TD: YFH: G: RGYHWMWDSRLFNNG: WEVLRYL LSNARWWLD. :
LNMFDGTDGHHYFHPGSRGYHWMWDSRLFNNGSWEVLRYL LSNARWWLDEY
^440 ^450 ^460 ^470 ^480
↖500 ↖510 ↖520 ↖530 ↖540
KFDGFRFDGVTSM MY IHHGLSVGFTGNYEEYFGLATDVDAVVY LMLVNDL
KFDGFRFDGVTSM MY. HHGL V: FTGNY. EYFGLATDV: AVVY: MLVNDL
KFDGFRFDGVTSM MYTHHGLQVSFTGNYSEYFGLATDVEAVVY MMLVNDL
^490 ^500 ^510 ^520 ^530
↖550 ↖560 ↖570 ↖580 ↖590
IHGLFPDAITIGEDVSGMPTFCIPVQEGGVGFDYRLHMAIADKRIELLKK
IHGLFP: A: : IGEDVSGMPTFC: P. Q: GG: GF: YRLHMA: ADK: IELLKK
IHGLFPEAVSIGEDVSGMPTFCLPTDGGIGFN YRLHMAVADKWIELLKK
^540 ^550 ^560 ^570 ^580
↖600 ↖610 ↖620 ↖630 ↖640
RDEDWRVGDIVHTLTNRRWSEKCVSYAESHDQALVGDKTIAFWLMDKDMY
: DEDWR: GDIVHTLTNRRW EKC V YAESHQALVGDKT: AFWLMDKDMY
QDEDWRMGDIVHTLTNRRWLEKCVVYAESHQALVGDKTLAFWLMDKDMY
^590 ^600 ^610 ^620 ^630
↖650 ↖660 ↖670 ↖680 ↖690
DFMALDRPSTSLIDRGIALHKMIRLVTMGLGGEGYLNFMGNEFGHPEWID
DFMALDRPST: LIDRGIALHKMIRL: TMGLGGEGYLNFMGNEFGHPEWID
DFMALDRPSTPLIDRGIALHKMIRLITMGLGGEGYLNFMGNEFGHPEWID
^640 ^650 ^660 ^670 ^680
↖700 ↖710 ↖720 ↖730 ↖740
FPRAEQHLSDGSVIPGNQFSYDKCRRRFDLGDAEYLR YRGLQEFDRPMQY
FPR: EQHL: : G. : : PGN: SYDKCRRRFDLGDA: YLR Y: G: QEFDR: MQ.
FPRGEQHLPNGKIVPGNNNSYDKCRRRFDLGDA DYLR YHGMQEFDRAMQH
^690 ^700 ^710 ^720 ^730
↖750 ↖760 ↖770 ↖780 ↖790
LECKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFWHTKSYSDYRIA
LE. Y. FMTSEHQ: ISRK: EGDR: I: FE: : NLVFNFWHT: SYSDY: :
LEETYGFMTSEHCYISRKNEGDRV IIFERDNLVFVFNFWHTNSYSDYKVG
^740 ^750 ^760 ^770 ^780
↖800 ↖810 ↖820 ↖830 ↖840
CLKPGKYKVALDSDDPLFGGFGRI DHNAEYFTFEGWYDDRPRS: MVYAPC
CLKPGKYK: LDSDD. LFGGF. R: : H. AEYFT EGWYDDRPRS: : VYAP
CLKPGKYKIVLDSDDTLFGGFNRLNHTAEYFTSEGWYDDRPRSFLVYAPS
^790 ^800 ^810 ^820 ^830
↖850 ↖860 ↖870
KTAVVYALVDKEEEEEEEEEEEVAA
: TAVVYAL. C E E E. : V :
PTAVVYALADGVESEPIELSDGVES
^840 ^850 ^860

1 11con.seq
1 19con.seq
1 10con.seq
45 psbe2con.seq
72 11con.seq
73 19con.seq
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165 psbe2con.seq
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189 10con.seq
274 psbe2con.seq
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551 11con.seq
551 19con.seq
49 10con.seq
634 psbe2con.seq
671 11con.seq
671 19con.seq
669 10con.seq
754 psbe2con.seq
791 11con.seq
791 19con.seq
789 10con.seq
874 psbe2con.seq

910 ACGCAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCAATAATGTGGATGGTCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGATGGACA 11con. seq
 911 ACGCAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCAATAATGTGGATGGTCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGATGGACA 19con. seq
 909 ACGCAATGCTGACTTATGACTCGGAATGAATTTGGTGTCTGAGATTTTCTGCAATAATGTGGATGGTCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGATGGACA 10con. seq
 994 ACGCAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCAATAATGTGGATGGTCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGATGGACA psbe2con. seq

 1030 CTCCATCAGGTGTTAAGGATTCATTCCTGCTTGATCAACTACTCTTTACAGCTTCCTGATGAATTCATATAATGGAATATATATATGATCCACCCGAAGAGAGGTATATCTTCC 11con. seq
 1031 CTCCATCAGGTGTTAAGGATTCATTCCTGCTTGATCAACTACTCTTTACAGCTTCCTGATGAATTCATATAATGGAATATGATATGATCCACCCGAAGAGAGGTATATCTTCC 19con. seq
 1029 CTCCATCAGGTGTTAAGGATTCATTCCTGCTTGATCAACTACTCTTTACAGCTTCCTGATGAATTCATATAATGGAATATATATGATCCACCCGAAGAGAGGTATATCTTCC 10con. seq
 1114 CTTCATCAGGTGTTAAGGATTCATTCCTGCTTGATCAACTACTCTTTACAGCTTCCTGATGAATTCATATAATGGAATATATATGATCCACCCGAAGAGAGGTATATCTTCC psbe2con. seq

 1150 AACACCCACGCCCAAGAAACCAAAAGTCGCTGAGAAATATATGAATCTCATATTGGAATGAGTAGTCGGAGCCTAAAATTAACCTACATCGTAATTTTAGAGATGAAGTTCTTCCTCGCA 11con. seq
 151 AACACCCACGCCCAAGAAACCAAAAGTCGCTGAGAAATATATGAATCTCATATTGGAATGAGTAGTCGGAGCCTAAAATTAACCTACATCGTAATTTTAGAGATGAAGTTCTTCCTCGCA 19con. seq
 1149 AACACCCACGCCCAAGAAACCAAAAGTCGCTGAGAAATATATGAATCTCATATTGGAATGAGTAGTCGGAGCCTAAAATTAACCTACATCGTAATTTTAGAGATGAAGTTCTTCCTCGCA 10con. seq
 1234 AACACCCACGCCCAAGAAACCAAAAGTCGCTGAGAAATATATGAATCTCATATTGGAATGAGTAGTCGGAGCCTAAAATTAACCTACATCGTAATTTTAGAGATGAAGTTCTTCCTCGCA psbe2con. seq

 1270 TAAAAAA-GCTTGGGTACAAAGCCGCTGCAATTTATGCTAGTTTGGTTATCATGTACAAAATTTTTTGGACCAAGCAGCCGTTTGGAAACGCC 11con. seq
 1271 TAAAAAA-GCTTGGGTACAAAGCCGCTGCAATTTATGCTAGTTTGGTTATCATGTACAAAATTTTTTGGACCAAGCAGCCGTTTGGAAACGCC 19con. seq
 1269 TAAAAAAAGCTTGGGTACAAAGCCGCTGCAATTTATGCTAGTTTGGTTATCATGTACAAAATTTTTTGGACCAAGCAGCCGTTTGGAAACGCC 10con. seq
 1354 TAAAAAAAGCTTGGGTACAAAGCCGCTGCAATTTATGCTAGTTTGGTTATCATGTACAAAATTTTTTGGACCAAGCAGCCGTTTGGAAACGCC psbe2con. seq

 1389 GACGACCTTAAGCTCTTGATGATGAAGCTCATGAGCTAGGAATTTGTTGTTCTCATGGACATCTGTTACAGCCATGCATCAAAATAACTTTAGATGGACTGAACATGTTTGACGGCACC 11con. seq
 1390 GACGACCTTAAGCTCTTGATGATGAAGCTCATGAGCTAGGAATTTGTTGTTCTCATGGACATCTGTTACAGCCATGCATCAAAATAACTTTAGATGGACTGAACATGTTTGACGGCACC 19con. seq
 1389 GACGACCTTAAGCTCTTGATGATGAAGCTCATGAGCTAGGAATTTGTTGTTCTCATGGACATCTGTTACAGCCATGCATCAAAATAACTTTAGATGGACTGAACATGTTTGACGGCACC 10con. seq
 1473 GACGACCTTAAGCTCTTGATGATGAAGCTCATGAGCTAGGAATTTGTTGTTCTCATGGACATCTGTTACAGCCATGCATCAAAATAACTTTAGATGGACTGAACATGTTTGACGGCACC psbe2con. seq

 1509 GATAGTGTGTAACCTTACCTTGGAGCTCGTGGTATCATATTGGATGAGGATTTCCGGCTCTTTAACTATGGAACCTGGAGGTACTTAGGTATCTTCTCAATGCGAGATGGTGGTIG 11con. seq
 1510 GATAGTGTGTAACCTTACCTTGGAGCTCGTGGTATCATATTGGATGAGGATTTCCGGCTCTTTAACTATGGAACCTGGAGGTACTTAGGTATCTTCTCAATGCGAGATGGTGGTIG 19con. seq
 09 GATAGTGTGTAACCTTACCTTGGAGCTCGTGGTATCATATTGGATGAGGATTTCCGGCTCTTTAACTATGGAACCTGGAGGTACTTAGGTATCTTCTCAATGCGAGATGGTGGTIG 10con. seq
 1593 GATAGTGTGTAACCTTACCTTGGAGCTCGTGGTATCATATTGGATGAGGATTTCCGGCTCTTTAACTATGGAACCTGGAGGTACTTAGGTATCTTCTCAATGCGAGATGGTGGTIG psbe2con. seq

 1628 GATGAGTTCAAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATACCTACCACCGGATATCGGTGGGATTCACCTGGGAACACGAGGAATACCTTTGGACTCGCAACTGAT 11con. seq
 1630 GATGATGTTCAAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATTTTACCCACCGGATATCGGTGGGATTCACCTGGGAACACGAGGAATACCTTTGGACTCGCAACTGAT 19con. seq
 1629 GATGAGTTCAAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATTTTACCTACCACCGGATATCGGTGGGATTCACCTGGGAACACGAGGAATACCTTTGGACTCGCAACTGAT 10con. seq
 1713 GATGAGTTCAAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATTTTACCTACCACCGGATATCGGTGGGATTCACCTGGGAACACGAGGAATACCTTTGGACTCGCAACTGAT psbe2con. seq

 1748 GTGGATGCTGTGTGATCTGATGCTGGTCAACGATCTTATTATCATAGGCTTTTCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCTGTTCAAGAT 11con. seq
 1750 GTGGATGCTGTGTGATCTGATGCTGGTCAACGATCTTATTATCATGGGCTTTTCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCTGTTCAAGAT 19con. seq
 1749 GTGGATGCTGTGTGATCTGATGCTGGTCAACGATCTTATTATCATGGGCTTTTCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCTGTTCAAGAT 10con. seq
 1833 GTGGATGCTGTGTGATCTGATGCTGGTCAACGATCTTATTATCATGGGCTTTTCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCTGTTCAAGAT psbe2con. seq

2795 **CTTGGTCAI** CACATAGAGCTTCTTGAC **ATCAGTCTGGCGGAATTG** CATGTGACAA **CAAGGTTTGCA** **CTCTTTCCACTATTAGTAGT** **CA** CGATATACGC 11con.seq
 2827 -----CIACATAGAGCTTCTTGACGTATCTGGCAATATTGGCAATCTGGCGGAATTTCATGTGACAG **-AAGGTTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGC** 19con.seq
 2814 -----C**ACATAGAGCTTCTTGACGTATCTGGCAATATTGGCAAT** **TAGTCTGGCGGAATTTCATGTGACAA** **-AAGGTTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGC** 10con.seq
 2895 -----CTACATAGAGCTTCTTGACGTATCTGGCAATATTGGCAATCTGGCGGAATTTCATGTGACAA **-AAGGTTTGCAATTCTTTCCACTATTAGTAGTGCAACGATATACGC** psbe2con.seq

2898 AGAGATGAAGTGTCTGAACAAA--CATATGTAAATCGATGAATTTATGTCGAATGCTGGACGATCGAATTCCTGCAGCC 11con.seq
 2937 AGAGATGAAGTGTCTGAACAAA--CATATGTAAATCGATGAATTTATGTCGAATGCTGGACGATCGAATTCCTGCAG 19con.seq
 2924 AGAGATGAAGTGTCTGAACAAA**AA**CATATGTAAATCGATGAATTTATGTCGAATGCTGGACGATCGAATTCCTGCAGCC 10con.seq
 3005 AGAGATGAAGTGTCTGAACAAA--CATATGTAAATCGATGAATTTATGTCGAATGCTGGACG**GGCTTCAG** **AGCTTTTGCTTAGTGAGTTCGTAAATTGTCATCTCTTANATGTACA** psbe2con.seq

2975 11con.seq
 3012 19con.seq
 3003 10con.seq
 3123 **GCCCACTAGAAATCAATTATGTGAGACCTAAAAACAATAACCATAAATGGAATAGTGTCTGATCTAATGATGTTTAAANCCNNNNAAAAAAAACCTCGAC** psbe2con.seq

Bgl II

GGATGCTAATGTTTCTGTATTCTTGAAAAAGCACTCTCTTTACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCGAATCCCGACC
CCTACGATTACAAAGACATAAGAACTTTTTCGTGAGAGAAAGTGCTTCTAGAACCGACTTTTCAGAAGAATGTTAAGGCTTAGGGCTGG
A N V S V F L K K H S L S R K I L A E K S S Y N S E S R P

TTCTACAGTTGCAGCATCGGGGAAAGTCTTGTGCCTGGAAYCCAGAGTGATAGCTCCTCATECTCAACAGACCAATTTGAGTTCACTGA
AAGATGTCAACGTCGTAGCCCTTTTCAGGAACACGGACCTTGGGTCTCACTATCGAGGAGTAGGAGTTGTCTGGTTAAACTCAAGTGACT
S T V A A S G K V L V P G ? Q S D S S S S S T O Q F E F T E

GACATCTCCAGAAAATTCCTCAGCATCAACTGATGTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAACTGAGAACGATGACGT
CTGTAGAGGTCTTTTAAGGGGTCGTAGTTGACTACATCTCAAGTTGTTACCTTGTGCGATCGGTCTAATTTTGACTCTTGCTACTGCA
T S P E N S P A S T O V D S S T M E H A S Q I K T E N D O V

TGAGCCGTCAAGTGATCTTACAGGAAGTGTGAAGAGCTGGATTTTGCTTCATCACTACAACACTACAAGAAGGTGGTAAACTGGAGGAGTC
ACTCGGCAGTTCACTAGAATGTCTTCACTTCTCGACCTAAACGAAGTAGTGATGTTGATGTTCTTCCACCATTTGACCTCCTCAG
E P S S D L T G S V E E L D F A S S L Q L Q E G G K L E E S

TAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAA
ATTTTGTAATTTATGAAGACTTCTCTGTTAATACTACTTAGACTATCTAGTCTCTCTCCCGTAGGGAGGTGGACCTGAACCACTCTT
K T L N T S E E T I I O E S D R I R E R G I P P P G L G Q K

Hinc II

GATTTATGAAATAGACCCCTTTTGACAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAACTGAGGGAGGCAATTGA
CTAAATACTTTATCTGGGGGAAACTGTTTGATAGCAGTTGTGGAACCTAATGTCCATAAGTGTGATGTTCTTTGACTCCCTCCGTAACT
I Y E I D P L L T N Y R Q H L D Y R Y S Q Y K K L R E A I D

HinD III

CAAGTATGAGGGTGGTTTGGGAAGCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTG
GTTCACTACTCCACCAAACTCTCGAAAAAGAGCACCAACTCTTTTACCCAAAGTGAGCATCAGGATGTCCATAGTGAATGGCACTCAC
K Y E G G L E A F S R G Y E K M G F T R S A T G I T Y R E W

Pvu II

GGCTCGTGGTGCCCACTCAGCTGCCCTCATTGAGAGATTTCAACAATTGGGACGCAAAATGCTGACATTATG4CTCGGAATGAATTTGGTGT
CCGAGGAGCCACGGGTGAGTCGACGGGAGTAACCTCTAAAGTTGTTAACCCTGCGTTTACGACTGTAATACTGAGCCTTACTTAAACCACA
A P G A Q S A A L I G D F N N W D A N A D I M T R N E F G V

CTGGGAGATTTTCTGCCAAATAATGTTGATGGTTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGYATGGACACTCCATCAGG
GACCTCTAAAAAGACGGTTTATTACACCTACCAAGAGGACGTTAAGGAGTACCCAGGTCTCACTTCTATGCTACCTGTGAGGTAGTCC
W E I F L P N N V D G S P A I P H G S R V K I R M D T P S G

TGTTA-33A-TTCAATTCCTGCTTGGATCAACTACTCTTTACAGCTTCTGATGAAA-TTCAATATAATGGAATATATTA-TGATCAACCCGA
ACAA-TTCTAAGGTAAAGGACGACCTAGTTGATGAGAAA-TTCAAGGACTACTTAAAGGTATATTACCTTATAAATACTAGG-TGGGCT
Y K D S I P A W I N Y S L Q L P D E I P Y N G I Y Y D P P E

AGAAGGAGAGGTATRTCTTCAACACCCACG33CCAAAGAAACCAAGTCTGCTGAGAATATA-TGAATCTCATATTGGAATGAGTAGTCCGGA
TCTCTCTCATAYAGAAGGTTGTGGGTGCCGGTTTCTTGGTTTCAAGCACTCTTATA-TACTTAGAGTATAACCTTACTCATCAGGCT
E E P Y ? F Q H P R P K K P K S L R I Y E S H I G M S S P E

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Xmn I

GCCTAAAATTAACATCATACGTGAATTTTAGAGATGAAGTTCTTCTCGCATAAAAAASCTTGGGTACAATGCGGTGCAAATTATGGCTAT 1080
CGGATTTTAAATTGAGTATGCACCTTAAATCTCTACTTCAAGAAGGAGCGTATTTTTTSGAACCCATGTTACGCCACGTTTAATACCGATA
P K I N S Y V N F R D E V L P R I K ? L G Y N A V Q I M A I
TCAAGASCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACGCCGACGACCTTAA 1170
AGTTCTCGTAAGAATAATACGATCAAAACCAATAGTACAGTGTAAAAAACGTTGTTCTGTCGGCAAAACCTTGCGGGCTGCTGGAATT
Q E H S Y Y A S F G Y H V T N F F A P S S R F G T P D D L K
GTCTTGGATGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTACAGCCATGCATCAAATAATACTTTAGATGGACT 1260
CAGAAACTAACTATTTTCGAGTACTCGATCCTTAAACAACAGAGTACCTGTAACAAGTGTGCGGTACGTAGTTTATTATGAAATCTACCTGA
S L I O K A H E L G I V V L M D I V H S H A S N N T L O G L

Sac I

GAACATGTTTGACGGCACAGATAGTTGTTACTTCTACTCTGGAGCTCGTGGTTATCATTGGATGTGGGATTCCCCTCTTTAACTATGG 1350
CTTGACAAACTGCCGTGTCTATCAACAATGAAAGTGAGACCTCGAGCACCAATAGTAACCTACACCTAAGGGCGGAGAAATTGATACC
N M F D G T O S C Y F H S G A R G Y H W M W D S R L F N Y G
AAACTGGGAGGTACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGTTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGAC 1440
TTTGACCTCCATGAATCCATAGAAGAGAGTTTACGCTCTACCACCAACCTACTCAAGTTTAAACTACCTAAATCTAAACTACCACACTG
N W E V L R Y L L S N A R W W L D E F K F D G F R F D G V T
ATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCAGTGGGAACACGAGGAATACCTTTGGACTCGCAACTGATGTGGATGCTGT 1530
TAGTTACTACATATGAGTGGTGCCTAATAGCCACCCTAAGTGACCTTGATGCTCCTTATGAAACCTGAGCGTTGACTACACCTACGACA
S M M Y T H H G L S V G F T G N Y E E Y F G L A T D V D A V

Hinc II

TGTGTATCTGATGCTGGTCAACGATCTTATTCACGGGCTTTTCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATT 1620
ACACATAGACTACGACCAAGTTGCTAGATAAAGTGCCCGAAAAGGGTCTACGTTAATGGTAACCACTTCTACAATCGCCTTACGGCTGTAA
V Y L M L V N D L I H G L F P D A I T I G E D V S G M P T F

Nde I

TTGTATTTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACG 1710
AACATAAGGGCAAGTTCTACCCCCACAACCGAAACTGATAGCCGACGTATACCGTTAACGACTATTTACCTAACTCAACGAGTTCTTTGC
C I P V Q D G G V G F D Y R L H M A I A D K W I E L L K K R
GGATGAGGATTGGAGAGTGGGTGATATTGTTTATACACTGACAAAAGAAGATGGTGGGAAAAGTGTGTTCATMCGCTGAAAGTCATGA 1800
CCTACTCCTAACCTCTCAGCCACTATAACAAGTATGTGACTGTTTATCTTCTACCAGCCCTTTACACAAAAGTAKGCGACTTCAGTACT
D E D W R V G D I V H T L T N R R W S E K C V S ? A E S H D

Hinc II

TCAGGCTTAGTCCGATATAAAATATAGCATCTCTGGCTGATGGACAGGATATGATGATTTTATGGCTCTGGATAGACCGTCAACATC 1890
AGTTGGAGATCAGCCACTATTTTGATATCTAPGACCGACTACCTGTTCTATACATACATAAATACCGAGACCTATCTGGCAGTTGTAG
D A L V G D K T I A ? W L M D K D M Y D F M A L D R P S T S

Aso 718
Kpn I

ATTAATAGATCGTGGGATAGCATTCACAAAGATGATTAGGCTTGAATATGGGATTAGGAGGAGAAGGGTACCTAAATTTCAATGGGAAA 1980
TAATTTATCTAGCACCTATCTTAACGTGTTCTACTAATCCGAACATTGATACCCCTAATCCTCCTCTTCCCATGGATTTAAAGTACCTTT
L I D R G I A L H K M I R L V T M G L G G E G Y L N F M G N

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EcoR I

TGAATTCGGGCCACCCCTGAGTGGATTGATTTCCCTAGGGCTGARCAACACCTCTCTGATGGCTCAGTAATTCCCGGAAACCAATTCAGTTA
ACTTAAGCCGGTGGGACTCACCTAACTAAAGGGATCCCGACTYGTGTGGAGAGACTACCGAGTCATTAAGGGCCTTTGGTTAAGTCAAT 2070
E F G H P E W I D F P R A E Q H L S D G S V I P G N Q F S Y

Ssp I

Nco I

TGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCATGGGTTGCAAGAATTTGACCGGGCTATGCAGTATCT 2160
ACTATTTACGTCTGCCTCTAAACTGGACCTCTACGTCTTATAAATTCTATGGTACCCAACGTTCTTAAACTGGCCCGATACGTCATAGA
D K C R R R F D L G D A E Y L R Y H G L Q E F D R A M Q Y L

TGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGGATGAAGGAGATAGGATGATTGTTATTTGAAARAGGAAA 2250
ACTTCTATTTATACTCAAATACTGAAGTCTTGGTCAAGTATAGTGCTTTCTACTTCTCTATCTACTAACATAAACTTTTCCTTT
E D K Y E F M T S E H Q F I S R K D E G D R M I V F E ? G N

CCTAGTTTTTGTCTTTAATTTTCACTGGACAAATAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAATACAAGGTTGGCTT 2340
GGATCAAAAACAGAAATTAAGTGACCTGTTTATCGATAAGTCTGATAGCGTATCCGACGGACTTCGGACCTTTTATGTTCCAACCGAA
L V F V F N F H W T N S Y S D Y R I G C L K P G K Y K V G L

Ssp I

GGACTCAGATGATCCACTTTTTTGGTGGCTTCGGGAGAA-TGATCATAATGCCGAATATTTACCTCTGAAGGATCGTATGATGATCGYCC 2430
CCTGAGTCTACTAGGTGAAAAACCACCGAAGCCCTCTTAAGTATTACGGCTTATAAAGTGGAGACTTCCTAGCATACTACTAGCRGG
D S D D P L F G G F G R I D H N A E Y F T S E G S Y D D R P

YCGYYCAATTATGGTGTATGCACCTAG-TAGAACAGCAGTGGTCTATGCACTAGTAGACAAANTAGAAGNAGAAGAAGAAGAAGAACCGN 2520
RGCRRGTAAATACCACATACGTGGATCATCTTGTGTCACCAGATACGTGATCATCTGTTTATCTTCNTCTTCTTCTTCTTCTTNGGCN
R ? I M V Y A P S R T A V V Y A L V D K ? E ? E E E E E ? ?

NGAAGAATTTT 2531
NCTTCTTAAAA
E E F

Fig. 9 (con)

18 / 31

| | | | | | | | | |
|-----|---------|---------|--------|--------|--------|---------|---------|--------------------------------------------------|
| | 10 | 20 | 30 | 40 | 50 | 60 | 70 | |
| 1 | -GATGGG | CCTTGA | ACTCAG | CAATTT | GACACT | CAGTTAG | TTACACT | CCATCACTTTATCAGATCTCTAT 10con. seq |
| 1 | TGATGGG | -CCTTGA | ACTCAG | CAATTT | GACACT | CAGTTAG | TTACACT | CCTATCACTTTATCAGATCTCTAT 11con. seq |
| 1 | TGATGGG | CCTTGA | ACTCAG | CAATTT | GACACT | CAGTTAG | TTACACT | CCTATCACTTTATCAGATCTCTAT 19con. seq |
| 1 | T | - | - | - | - | - | - | 86CON. SEQ |
| 1 | - | - | - | - | - | - | - | pcrsbe2con. seq |
| | 80 | 90 | 100 | 110 | 120 | 130 | 140 | |
| 69 | TTTTCT | CTTAAT | TCCAAC | CAAGG | -AATGA | ATAAAA | AGATAG | ATTGTAAAAACCTAAGGAGAGAAGAA 10con. seq |
| 70 | TTTTCT | CTTAAT | TCCAAC | CAAGG | -AATGA | ATAAAA | AGGATAG | ATTGTAAAAACCTAAGGAGAGAAGAA 11con. seq |
| 71 | TTTTCT | CTTAAT | TCCAAC | CAAGG | -AATGA | ATAAAA | AGGATAG | ATTGTAAAAACCTAAGGAGAGAAGAA 19con. seq |
| 7 | - | - | - | - | - | - | - | 86CON. SEQ |
| 1 | - | - | - | - | - | - | - | pcrsbe2con. seq |
| | 150 | 160 | 170 | 180 | 190 | 200 | 210 | |
| 138 | GAAAGAT | GGTGTA | TACACT | CTCTGG | AGTTCT | TTTTCT | ACTGTT | CCATCAGTGTAACAAATCTAATGGATT 10con. seq |
| 140 | GAAAGAT | GGTGTA | TACTCT | CTGG | AGTTCT | TTTTCT | ACTGTT | CCATCAGTGTAACAAATCTAATGGATT 11con. seq |
| 140 | GAAAGAT | GGTGTA | TACACT | CTCTGG | AGTTCT | TTTTCT | ACTGTT | CCATCAGTGTAACAAATCTAATGGATT 19con. seq |
| 33 | - | - | - | - | - | - | - | 86CON. SEQ |
| 1 | - | - | - | - | - | - | - | pcrsbe2con. seq |
| | 220 | 230 | 240 | 250 | 260 | 270 | 280 | |
| 208 | CAGCAGT | AATGGT | GATCGG | AGGAAT | GCTAAT | ATTTCT | GTAATC | TTTGAAAAACACTCTCTTTACGGAAG 10con. seq |
| 210 | CAGCAGT | AATGGT | GATCGG | AGGAAT | GCTAAT | ATTTCT | GTAATC | TTTGAAAAAGCACTCTCTTTACGGAAG 11con. seq |
| 210 | CAGCAGT | AATGGT | GATCGG | AGGAAT | GCTAAT | ATTTCT | GTAATC | TTTGAAAAAGCACTCTCTTTACGGAAG 19con. seq |
| 48 | CA | - | - | - | - | - | - | 86CON. SEQ |
| 1 | - | - | - | - | - | - | - | pcrsbe2con. seq |
| | 290 | 300 | 310 | 320 | 330 | 340 | 350 | |
| 278 | ATCTTGG | CTGAAA | AGTCTT | CTTACA | AATTCG | GAATCC | GACCTT | CTACAGTTGCAGCATCGGGGAAAGTCC 10con. seq |
| 280 | ATCTTGG | CTGAAA | AGTCTT | CTTACA | AATTCG | GAATCC | GACCTT | CTACAGTTGCAGCATCGGGGAAAGTCC 11con. seq |
| 280 | ATCTTGG | CTGAAA | AGTCTT | CTTACA | AATTCG | GAATCC | GACCTT | CTACAGTTGCAGCATCGGGGAAAGTCC 19con. seq |
| 57 | ATCTTGG | CTGAAA | AGTCTT | CTTACA | AATTCG | GAATCC | GACCTT | CTACAGTTGCAGCATCGGGGAAAGTCC 86CON. SEQ |
| 50 | ATCTTGG | CTGAAA | AGTCTT | CTTACA | AATTCG | GAATCC | GACCTT | CTACAGTTGCAGCATCGGGGAAAGTCC pcrsbe2con. seq |
| | 360 | 370 | 380 | 390 | 400 | 410 | 420 | |
| 348 | TTGTGCT | TGGAA | CCAGAG | TGAT | AGCTCT | CATCCT | CAACAG | AAATTTGAGTTCTGAGACATCTCC 10con. seq |
| 350 | TTGTGCT | TGGAA | CCAGAG | TGAT | AGCTCT | CATCCT | CAACAG | AAATTTGAGTTCTGAGACATCTCC 11con. seq |
| 350 | TTGTGCT | TGGAA | CCAGAG | TGAT | AGCTCT | CATCCT | CAACAG | AAATTTGAGTTCTGAGACATCTCC 19con. seq |
| 127 | TTGTGCT | TGGAA | CCAGAG | TGAT | AGCTCT | CATCCT | CAACAG | AAATTTGAGTTCTGAGACATCTCC 86CON. SEQ |
| 120 | TTGTGCT | TGGAA | CCAGAG | TGAT | AGCTCT | CATCCT | CAACAG | AAATTTGAGTTCTGAGACATCTCC pcrsbe2con. seq |
| | 430 | 440 | 450 | 460 | 470 | 480 | 490 | |
| 418 | AGAAAA | ATCCCC | AGCATC | AACTG | ATGAT | AGTTCA | ACAAT | GGAACACGCTAGCCAGATTAAACTGAG 10con. seq |
| 420 | AGAAAA | ATCCCC | AGCATC | AACTG | ATGAT | AGTTCA | ACAAT | GGAACACGCTAGCCAGATTAAACTGAG 11con. seq |
| 420 | AGAAAA | ATCCCC | AGCATC | AACTG | ATGAT | AGTTCA | ACAAT | GGAACACGCTAGCCAGATTAAACTGAG 19con. seq |
| 197 | AGAAAA | ATCCCC | AGCATC | AACTG | ATGAT | AGTTCA | ACAAT | GGAACACGCTAGCCAGATTAAACTGAG 86CON. SEQ |
| 190 | AGAAAA | ATCCCC | AGCATC | AACTG | ATGAT | AGTTCA | ACAAT | GGAACACGCTAGCCAGATTAAACTGAG pcrsbe2con. seq |
| | 500 | 510 | 520 | 530 | 540 | 550 | 560 | |
| 488 | AACGAT | GACCT | TGAG | CCGTCA | AGTGAT | CTTAC | AGGAAG | TGTGAAGAGCTGGATTTTGGTTTCACTACTAC 10con. seq |
| 490 | AACGAT | GACCT | TGAG | CCGTCA | AGTGAT | CTTAC | AGGAAG | TGTGAAGAGCTGGATTTTGGTTTCACTACTAC 11con. seq |
| 490 | AACGAT | GACCT | TGAG | CCGTCA | AGTGAT | CTTAC | AGGAAG | TGTGAAGAGCTGGATTTTGGTTTCACTACTAC 19con. seq |
| 267 | AACGAT | GACCT | TGAG | CCGTCA | AGTGAT | CTTAC | AGGAAG | TGTGAAGAGCTGGATTTTGGTTTCACTACTAC 86CON. SEQ |
| 260 | AACGAT | GACCT | TGAG | CCGTCA | AGTGAT | CTTAC | AGGAAG | TGTGAAGAGCTGGATTTTGGTTTCACTACTAC pcrsbe2con. seq |
| | 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| 558 | AACGAT | GACCT | TGAG | CCGTCA | AGTGAT | CTTAC | AGGAAG | TGTGAAGAGCTGGATTTTGGTTTCACTACTAC 10con. seq |
| 560 | AACGAT | GACCT | TGAG | CCGTCA | AGTGAT | CTTAC | AGGAAG | TGTGAAGAGCTGGATTTTGGTTTCACTACTAC 11con. seq |
| 580 | AACGAT | GACCT | TGAG | CCGTCA | AGTGAT | CTTAC | AGGAAG | TGTGAAGAGCTGGATTTTGGTTTCACTACTAC 19con. seq |
| 337 | AACGAT | GACCT | TGAG | CCGTCA | AGTGAT | CTTAC | AGGAAG | TGTGAAGAGCTGGATTTTGGTTTCACTACTAC 86CON. SEQ |
| 330 | AACGAT | GACCT | TGAG | CCGTCA | AGTGAT | CTTAC | AGGAAG | TGTGAAGAGCTGGATTTTGGTTTCACTACTAC pcrsbe2con. seq |

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| | | | | | | | | |
|------|---------------------------------------------------------------------------|------|------|------|------|------|------|-----------------|
| | 640 | 650 | 660 | 670 | 680 | 690 | 700 | |
| 628 | ATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCC | | | | | | | 10con. seq |
| 630 | ATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCC | | | | | | | 11con. seq |
| 630 | ATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCC | | | | | | | 19con. seq |
| 407 | ATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCC | | | | | | | 86CON. SEQ |
| 400 | ATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAAATAGACCCC | | | | | | | pcrsbe2con. seq |
| | 710 | 720 | 730 | 740 | 750 | 760 | 770 | |
| 696 | CTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAACTGAGGGAGGCAATTG | | | | | | | 10con. seq |
| 700 | CTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAACTGAGGGAGGCAATTG | | | | | | | 11con. seq |
| 700 | CTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAACTGAGGGAGGCAATTG | | | | | | | 19con. seq |
| 477 | CTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAACTGAGGGAGGCAATTG | | | | | | | 86CON. SEQ |
| 470 | CTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAACTGAGGGAGGCAATTG | | | | | | | pcrsbe2con. seq |
| | 780 | 790 | 800 | 810 | 820 | 830 | 840 | |
| 768 | ACAAGTATGAGGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTAC | | | | | | | 10con. seq |
| 770 | ACAAGTATGAGGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTAC | | | | | | | 11con. seq |
| 770 | ACAAGTATGAGGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTAC | | | | | | | 19con. seq |
| 547 | ACAAGTATGAGGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTAC | | | | | | | 86CON. SEQ |
| 540 | ACAAGTATGAGGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAGTGCTAC | | | | | | | pcrsbe2con. seq |
| | 850 | 860 | 870 | 880 | 890 | 900 | 910 | |
| 838 | AGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCAGTCAGCTGCCCTCATTGGGAGATTTCACCAATTGG | | | | | | | 10con. seq |
| 839 | AGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCAGTCAGCTGCCCTCATTGGGAGATTTCACCAATTGG | | | | | | | 11con. seq |
| 840 | AGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCAGTCAGCTGCCCTCATTGGGAGATTTCACCAATTGG | | | | | | | 19con. seq |
| 617 | AGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCAGTCAGCTGCCCTCATTGGGAGATTTCACCAATTGG | | | | | | | 86CON. SEQ |
| 610 | AGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCAGTCAGCTGCCCTCATTGGGAGATTTCACCAATTGG | | | | | | | pcrsbe2con. seq |
| | 920 | 930 | 940 | 950 | 960 | 970 | 980 | |
| 908 | GACGCAAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGG | | | | | | | 10con. seq |
| 909 | GACGCAAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGG | | | | | | | 11con. seq |
| 910 | GACGCAAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGG | | | | | | | 19con. seq |
| 687 | GACGCAAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGG | | | | | | | 86CON. SEQ |
| 680 | GACGCAAAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGG | | | | | | | pcrsbe2con. seq |
| | 990 | 1000 | 1010 | 1020 | 1030 | 1040 | 1050 | |
| 978 | ATGGTTCTCCTGCAATTCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGA | | | | | | | 10con. seq |
| 979 | ATGGTTCTCCTGCAATTCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGA | | | | | | | 11con. seq |
| 980 | ATGGTTCTCCTGCAATTCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGA | | | | | | | 19con. seq |
| 757 | ATGGTTCTCCTGCAATTCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGA | | | | | | | 86CON. SEQ |
| 750 | ATGGTTCTCCTGCAATTCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGA | | | | | | | pcrsbe2con. seq |
| | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 | |
| 1048 | TTCCATTCTCTGCTTGGATCAACTACTCTTTACAGCTTCTTGATGAAATTCATATAATGGAATATATTAT | | | | | | | 10con. seq |
| 1049 | TTCCATTCTCTGCTTGGATCAACTACTCTTTACAGCTTCTTGATGAAATTCATATAATGGAATATATTAT | | | | | | | 11con. seq |
| 1050 | TTCCATTCTCTGCTTGGATCAACTACTCTTTACAGCTTCTTGATGAAATTCATATAATGGAATATATTAT | | | | | | | 19con. seq |
| 827 | TTCCATTCTCTGCTTGGATCAACTACTCTTTACAGCTTCTTGATGAAATTCATATAATGGAATATATTAT | | | | | | | 86CON. SEQ |
| 820 | TTCCATTCTCTGCTTGGATCAACTACTCTTTACAGCTTCTTGATGAAATTCATATAATGGAATATATTAT | | | | | | | pcrsbe2con. seq |
| | 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | |
| 1118 | GATCCACCCGAGAGGAGAGGATATCTTCCAAACACCCACGGCCAAAGAAACCAAGTCGCTGAGAATAT | | | | | | | 10con. seq |
| 1119 | GATCCACCCGAGAGGAGAGGATATCTTCCAAACACCCACGGCCAAAGAAACCAAGTCGCTGAGAATAT | | | | | | | 11con. seq |
| 1120 | GATCCACCCGAGAGGAGAGGATATCTTCCAAACACCCACGGCCAAAGAAACCAAGTCGCTGAGAATAT | | | | | | | 19con. seq |
| 895 | GATCCACCCGAGAGGAGAGGATATCTTCCAAACACCCACGGCCAAAGAAACCAAGTCGCTGAGAATAT | | | | | | | 86CON. SEQ |
| 890 | GATCCACCCGAGAGGAGAGGATATCTTCCAAACACCCACGGCCAAAGAAACCAAGTCGCTGAGAATAT | | | | | | | pcrsbe2con. seq |
| | 1200 | 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | |
| 1188 | ATGAAATCTCTATTTGGAATGAGTAGTCCCGAGGCTAAAAATTAACCTCATACGTGAAATTTAGAGATGAAGT | | | | | | | 10con. seq |
| 1189 | ATGAAATCTCTATTTGGAATGAGTAGTCCCGAGGCTAAAAATTAACCTCATACGTGAAATTTAGAGATGAAGT | | | | | | | 11con. seq |
| 1190 | ATGAAATCTCTATTTGGAATGAGTAGTCCCGAGGCTAAAAATTAACCTCATACGTGAAATTTAGAGATGAAGT | | | | | | | 19con. seq |
| 965 | ATGAAATCTCTATTTGGAATGAGTAGTCCCGAGGCTAAAAATTAACCTCATACGTGAAATTTAGAGATGAAGT | | | | | | | 86CON. SEQ |
| 960 | ATGAAATCTCTATTTGGAATGAGTAGTCCCGAGGCTAAAAATTAACCTCATACGTGAAATTTAGAGATGAAGT | | | | | | | pcrsbe2con. seq |

| | 1270 | 1280 | 1290 | 1300 | 1310 | 1320 | 1330 | |
|------|-------------------------------------------------------------------------|-----------------------------------------------------|-------------------------------------|------|------|------|------|-----------------|
| 1258 | TCTTCCTCGCATAAAAAA | AGCTTGGGTACAATGCG | GTGCAAATTATGGCTATTCAAGAGCATTCTTATTA | | | | | 10con. seq |
| 1259 | TCTTCCTCGCATAAAAAA | GCTTGGGTACAATGCGCTGCCAATTATGGCTATTCAAGAGCATTCTTATTA | | | | | | 11con. seq |
| 1260 | TCTTCCTCGCATAAAAAA | GCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTA | | | | | | 19con. seq |
| 1035 | TCTTCCTCGCATAAAAAA | GCTTGGGTACAATGCGCTGCAAATTATGGCTATTCAAGAGCATTCTTATTA | | | | | | 86CON. SEQ |
| 1030 | TCTTCCTCGCATAAAAAA | GCTTGGGTACAATGCGGTGCAAATTATGGCTATTCAAGAGCATTCTTATTA | | | | | | pcrsbe2con. seq |
| | 1340 | 1350 | 1360 | 1370 | 1380 | 1390 | 1400 | |
| 1328 | TGCTAGTTTTGGTTATCATGT | CACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACGCCGACGACCTT | | | | | | 10con. seq |
| 1328 | TGCTAGTTTTGGTTATCATGT | CACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACGCCGACGACCTT | | | | | | 11con. seq |
| 1329 | TGCTAGTTTTGGTTATCATGT | CACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACGCCGACGACCTT | | | | | | 19con. seq |
| 1104 | TGCTAGTTTTGGTTATCATGT | CACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACGCCGACGACCTT | | | | | | 86CON. SEQ |
| 1099 | TGCTAGTTTTGGTTATCATGT | CACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACGCCGACGACCTT | | | | | | pcrsbe2con. seq |
| | 1410 | 1420 | 1430 | 1440 | 1450 | 1460 | 1470 | |
| 1398 | AAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTACAGCCATGCAT | | | | | | | 10con. seq |
| 1398 | AAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTACAGCCATGCAT | | | | | | | 11con. seq |
| 1399 | AAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTACAGCCATGCAT | | | | | | | 19con. seq |
| 1174 | AAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTACAGCCATGCAT | | | | | | | 86CON. SEQ |
| 1169 | AAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTACAGCCATGCAT | | | | | | | pcrsbe2con. seq |
| | 1480 | 1490 | 1500 | 1510 | 1520 | 1530 | 1540 | |
| 1468 | CAAATAAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCG | | | | | | | 10con. seq |
| 1468 | CAAATAAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCG | | | | | | | 11con. seq |
| 1469 | CAAATAAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCG | | | | | | | 19con. seq |
| 1244 | CAAATAAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCG | | | | | | | 86CON. SEQ |
| 1239 | CAAATAAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCG | | | | | | | pcrsbe2con. seq |
| | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 | 1610 | |
| 1538 | TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAGCTGGGAGGTACTTAGGTATCTTCTC | | | | | | | 10con. seq |
| 1538 | TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAGCTGGGAGGTACTTAGGTATCTTCTC | | | | | | | 11con. seq |
| 1539 | TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAGCTGGGAGGTACTTAGGTATCTTCTC | | | | | | | 19con. seq |
| 1314 | TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAGCTGGGAGGTACTTAGGTATCTTCTC | | | | | | | 86CON. SEQ |
| 1309 | TGGTTATCATTGGATGTGGGATTCCCGCCTCTTTAACTATGGAAGCTGGGAGGTACTTAGGTATCTTCTC | | | | | | | pcrsbe2con. seq |
| | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 | |
| 1608 | TCAAATGCGAGATGGTGGTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGA | | | | | | | 10con. seq |
| 1607 | TCAAATGCGAGATGGTGGTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGA | | | | | | | 11con. seq |
| 1609 | TCAAATGCGAGATGGTGGTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGA | | | | | | | 19con. seq |
| 1384 | TCAAATGCGAGATGGTGGTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGA | | | | | | | 86CON. SEQ |
| 1379 | TCAAATGCGAGATGGTGGTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGA | | | | | | | pcrsbe2con. seq |
| | 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | |
| 1673 | TGTATCTCACCACGGATTATCGGTGGGATTCACTGGGAACACGAGGAATACTTTGGACTCGCAACTGA | | | | | | | 10con. seq |
| 1677 | TGTATCTCACCACGGATTATCGGTGGGATTCACTGGGAACACGAGGAATACTTTGGACTCGCAACTGA | | | | | | | 11con. seq |
| 1679 | TGTATCTCACCACGGATTATCGGTGGGATTCACTGGGAACACGAGGAATACTTTGGACTCGCAACTGA | | | | | | | 19con. seq |
| 1454 | TGTATCTCACCACGGATTATCGGTGGGATTCACTGGGAACACGAGGAATACTTTGGACTCGCAACTGA | | | | | | | 86CON. SEQ |
| 1449 | TGTATCTCACCACGGATTATCGGTGGGATTCACTGGGAACACGAGGAATACTTTGGACTCGCAACTGA | | | | | | | pcrsbe2con. seq |
| | 1760 | 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | |
| 1748 | TGTGGATGCTGTGTGTATCTGATGCTGGTCAACGATCTATTCACTGGGCTTTCCAGATGCAATTACC | | | | | | | 10con. seq |
| 1747 | TGTGGATGCTGTGTGTATCTGATGCTGGTCAACGATCTATTCACTGGGCTTTCCAGATGCAATTACC | | | | | | | 11con. seq |
| 1749 | TGTGGATGCTGTGTGTATCTGATGCTGGTCAACGATCTATTCACTGGGCTTTCCAGATGCAATTACC | | | | | | | 19con. seq |
| 1524 | TGTGGATGCTGTGTGTATCTGATGCTGGTCAACGATCTATTCACTGGGCTTTCCAGATGCAATTACC | | | | | | | 86CON. SEQ |
| 1519 | TGTGGATGCTGTGTGTATCTGATGCTGGTCAACGATCTATTCACTGGGCTTTCCAGATGCAATTACC | | | | | | | pcrsbe2con. seq |
| | 1830 | 1840 | 1850 | 1860 | 1870 | 1880 | 1890 | |
| 1813 | ATTGGTGAAGAATTAGCGGAAATGCGGACATTTGTATTTCCGCTTTCAAGAAGGGGGTGTGGCTTTGACT | | | | | | | 10con. seq |
| 1817 | ATTGGTGAAGAATTAGCGGAAATGCGGACATTTGTATTTCCGCTTTCAAGAAGGGGGTGTGGCTTTGACT | | | | | | | 11con. seq |
| 1819 | ATTGGTGAAGAATTAGCGGAAATGCGGACATTTGTATTTCCGCTTTCAAGAAGGGGGTGTGGCTTTGACT | | | | | | | 19con. seq |
| 1894 | ATTGGTGAAGAATTAGCGGAAATGCGGACATTTGTATTTCCGCTTTCAAGAAGGGGGTGTGGCTTTGACT | | | | | | | 86CON. SEQ |
| 1889 | ATTGGTGAAGAATTAGCGGAAATGCGGACATTTGTATTTCCGCTTTCAAGAAGGGGGTGTGGCTTTGACT | | | | | | | pcrsbe2con. seq |

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|------|--------------------------------------------------------------------------|------|------|------|------|------|-----------------|--|
| | 2530 | 2540 | 2550 | 2560 | 2570 | 2580 | 2590 | |
| 2518 | ATTCAGACTATCGCATAGGCTGCCGGAAGCCTGGAAAAATACAAGGTTGCCCTTGGACTCAGATGATCCACT | | | | | | 10con. seq | |
| 2517 | ATTCAGACTATCGCATAGGCTGCCGGAAGCCTGGAAAAATACAAGGTTGCCCTTGGACTCAGATGATCCACT | | | | | | 11con. seq | |
| 2519 | ATTCAGACTATCGCATAGGCTGCCGGAAGCCTGGAAAAATACAAGGTTGCCCTTGGACTCAGATGATCCACT | | | | | | 19con. seq | |
| 2294 | ATTCAGACTATCGCATAGGCTGCCGGAAGCCTGGAAAAATACAAGGTTGCCCTTGGACTCAGATGATCCACT | | | | | | 86CON. SEQ | |
| 2289 | ATTCAGACTATCGCATAGGCTGCCGGAAGCCTGGAAAAATACAAGGTTGCCCTTGGACTCAGATGATCCACT | | | | | | pcrsbe2con. seq | |

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|------|-----------------------------------------------------------------------|------|------|------|-------|-------|-----------------|--|
| | 2600 | 2610 | 2620 | 2630 | *2640 | *2650 | 2660 | |
| 2586 | TTTGGTGGCTTCGGGAGAATTGATCATATATGCCGAATATTTACCTTTGAAGGATGGTATGATGATCGT | | | | | | 10con. seq | |
| 2587 | TTTGGTGGCTTCGGGAGAATTGATCATATATGCCGAATATTTACCTTTGAAGGATGGTATGATGATCGT | | | | | | 11con. seq | |
| 2589 | TTTGGTGGCTTCGGGAGAATTGATCATATATGCCGAATATTTACCTTTGAAGGATGGTATGATGATCGT | | | | | | 19con. seq | |
| 2364 | TTTGGTGGCTTCGGGAGAATTGATCATATATGCCGAATATTTACCTTTGAAGGATGGTATGATGATCGT | | | | | | 86CON. SEQ | |
| 2359 | TTTGGTGGCTTCGGGAGAATTGATCATATATGCCGAATATTTACCTTTGAAGGATGGTATGATGATCGT | | | | | | pcrsbe2con. seq | |

| | | | | | | | | |
|------|------------------------------------------------------------------|------|-------|------|------|------|-----------------|--|
| | 2670 | 2680 | *2690 | 2700 | 2710 | 2720 | 2730 | |
| 2658 | CCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAG | | | | | | 10con. seq | |
| 2657 | CCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAG | | | | | | 11con. seq | |
| 2659 | CCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAG | | | | | | 19con. seq | |
| 2434 | CCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAG | | | | | | 86CON. SEQ | |
| 2429 | CCTCGTTCAATTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAG | | | | | | pcrsbe2con. seq | |

| | | | | | | | | |
|------|------------------------------------------------------------------------|------|------|------|------|------|-----------------|--|
| | 2740 | 2750 | 2760 | 2770 | 2780 | 2790 | 2800 | |
| 2722 | AAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAA | | | | | | 10con. seq | |
| 2722 | AAGAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAA | | | | | | 11con. seq | |
| 2729 | AAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAA | | | | | | 19con. seq | |
| 2501 | AAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAA | | | | | | 86CON. SEQ | |
| 2499 | AAGAAGAAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAATGAACGAA | | | | | | pcrsbe2con. seq | |

| | | | | | | | | |
|------|-------------------------------------------------------------------------|------|------|------|------|------|-----------------|--|
| | 2810 | 2820 | 2830 | 2840 | 2850 | 2860 | 2870 | |
| 2786 | CTTGATGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACGTATCTGGCAATATTGCATCAGT | | | | | | 10con. seq | |
| 2784 | CTTGATGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACGTATCTGGCAATATTGCATCAGT | | | | | | 11con. seq | |
| 2799 | CTTGATGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACGTATCTGGCAATATTGCATCAGT | | | | | | 19con. seq | |
| 2571 | CTTGATGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACGTATCTGGCAATATTGCATCAGT | | | | | | 86CON. SEQ | |
| 2529 | CTTGATGATCGCGTTGAAAGATTTGAACGCTACATAGAGCTTCTTGACGTATCTGGCAATATTGCATCAGT | | | | | | pcrsbe2con. seq | |

| | | | | | | | | |
|------|------------------------------------------------------------------------|------|------|------|------|------|-----------------|--|
| | 2880 | 2890 | 2900 | 2910 | 2920 | 2930 | 2940 | |
| 2856 | CTTGCGCGAATTTTCATGTGACAACAAGGTTTGCATTTCTTCCACTATTAGTAGTGCAACGATATACGCA | | | | | | 10con. seq | |
| 2829 | CTTGCGCGAATTTTCATGTGACAACAAGGTTTGCATTTCTTCCACTATTAGTAGTGCAACGATATACGCA | | | | | | 11con. seq | |
| 2869 | CTTGCGCGAATTTTCATGTGACAACAAGGTTTGCATTTCTTCCACTATTAGTAGTGCAACGATATACGCA | | | | | | 19con. seq | |
| 2576 | CTTGCGCGAATTTTCATGTGACAACAAGGTTTGCATTTCTTCCACTATTAGTAGTGCAACGATATACGCA | | | | | | 86CON. SEQ | |
| 2529 | CTTGCGCGAATTTTCATGTGACAACAAGGTTTGCATTTCTTCCACTATTAGTAGTGCAACGATATACGCA | | | | | | pcrsbe2con. seq | |

| | | | | | | | | |
|------|-----------------------------------------------------------------------|------|------|------|------|------|-----------------|--|
| | 2950 | 2960 | 2970 | 2980 | 2990 | 3000 | 3010 | |
| 2925 | GAGATGAAGTGTGAAACAAAATGATAATGAAAATCGATGAATTTATGTGCAATGCTGGGACGATCGAAT | | | | | | 10con. seq | |
| 2899 | GAGATGAAGTGTGAAACAAAATGATAATGAAAATCGATGAATTTATGTGCAATGCTGGGACGATCGAAT | | | | | | 11con. seq | |
| 2938 | GAGATGAAGTGTGAAACAAAATGATAATGAAAATCGATGAATTTATGTGCAATGCTGGGACGATCGAAT | | | | | | 19con. seq | |
| 2576 | GAGATGAAGTGTGAAACAAAATGATAATGAAAATCGATGAATTTATGTGCAATGCTGGGACGATCGAAT | | | | | | 86CON. SEQ | |
| 2529 | GAGATGAAGTGTGAAACAAAATGATAATGAAAATCGATGAATTTATGTGCAATGCTGGGACGATCGAAT | | | | | | pcrsbe2con. seq | |

| | | | | | | | | |
|------|---------|------|---------|--|---------|--|-----------------|--|
| | 3020 | 3030 | | | | | | |
| 2995 | GCTGCAG | | GCTGCAG | | GCTGCAG | | 10con. seq | |
| 2987 | GCTGCAG | | GCTGCAG | | GCTGCAG | | 11con. seq | |
| 3006 | GCTGCAG | | GCTGCAG | | GCTGCAG | | 19con. seq | |
| 2576 | GCTGCAG | | GCTGCAG | | GCTGCAG | | 86CON. SEQ | |
| 2529 | GCTGCAG | | GCTGCAG | | GCTGCAG | | pcrsbe2con. seq | |

Fig. 10 (con.) 23/31

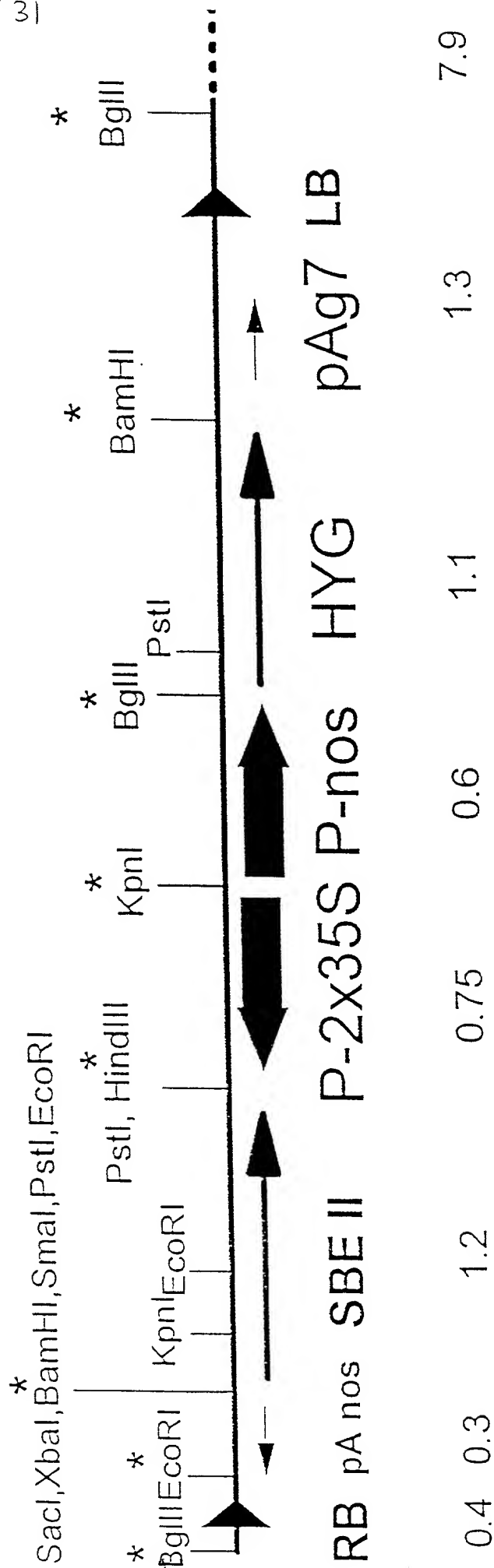


fig. 11

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TCATTAAAGAGGAGAAATTAACATGAGAGGATCTCACCATCACCATCACCATGGGATCT 60
AGTAATTTCTCCTCTTTAATTGATACTCTCCTAGAGTGGTAGTGGTAGTGGTACCCTAGA
M R G S H H H H H G I

Nco I
BstX I

EcoR I

TGGCTGAAAAGTCTTCTTACAATTCCGAATTCCGACCTTCTACAGTTGCAGCATCGGGGA 120
ACCGACTTTTTCAGAAGAATGTTAAGGCTTAAGGCTGGAAGATGTCAACGTCGTAGCCCCCT
L A E K S S Y N S E F R P S T V A A S G

AAGTCCTTGTGCCTGGAACCCAGAGTGATAGCTCCTCATCCTCAACAAACCAATTTGAGT 180
TTCAGGAACACGGACCTTGGGTCTCACTATCGAGGAGTAGGAGTTGTTTGGTTAACTCA
K V L V P G T Q S D S S S S S T N Q F E

TCACTGAGACATCTCCAGAAAATTCCCCAGCATCAACTGATGTAGATAGTTCAACAATGG 240
AGTGACTCTGTAGAGGTCTTTTAAGGGGTCGTAGTTGACTACATCTATCAAGTTGTTACC
F T E T S P E N S P A S T D V D S S T M

AACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAGCCGTCAAGTGATCTTACAG 300
TTGTGCGATCGGTCTAATTTTGACTCTTGCTACTGCAACTCGGCAGTTCACTAGAATGTC
E H A S Q I K T E N D D V E P S S D L T

GAAGTGTTGAAGAGCTGGATTTTGCTTCATCACTACAACCTACAAGAAGGTGGTAAACTGG 360
CTTCACAACTTCTCGACCTAAAACGAAGTAGTGATGTTGATGTTCTTCCACCATTGACC
G S V E E L D F A S S L Q L Q E G G K L

AGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATCTGATAGGATCA 420
TCCTCAGATTTTGTAAATTTATGAAGACTTCTCTGTTAATAACTACTTAGACTATCCTAGT
E E S K T L N T S E E T I I D E S D R I

GAGAGAGGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTATGAAATAGACCCCTTT 480
CTCTCTCCCCGTAGGGAGGTGGACCTGAACCAAGTCTTCTAAATACTTTATCTGGGGGAAA
R E R G I P P P G L G Q K I V E I D P L

Hinc II

TGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAACTGAGGGAGG
ACTGTTTGATAGCAGTTGTGGAACCTAATGTCCATAAGTGTGTCATGTTCTTTGACTCCCTCC
L T N Y R Q H L D Y R Y S Q Y K K L R E

HinD III

CAATTGACAAGTATGAGGGTGGTTTGGAAAGCTTTTTCTCGTGGTTATGAAAAATGGGTT
GTAACTGTTTCATACTCCACCAAACCTTCGAAAAAGAGCACCAATACTTTTTTACCCAA
A I D K Y E G G L E A F S R G Y E K M G

Pvu II

TCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCAGTCAGCTG
AGTGAGCATCACGATGTCCATAGTGAATGGCACTCACCCGAGGACCACGGGTCAGTCGAC
F T R S A T G I T Y R E W A P G A Q S A

CCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGACTCGGAATGAAT
GGGAGTAACCTCTAAAGTTGTTAACCCTGCGTTTACGACTGTAATACTGAGCCTTACTTA
A L I G D F N N W D A N A D I M T R N E

TTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGCAATTCCTCATG
AACCACAGACCTCTAAAAAGACGGTTTATTACACCTACCAAGAGGACGTTAAGGAGTAC
F G V W E I F L P N N V D G S P A I P H

SnaB I

GGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCCATTCTGCTT
CCAGGTCTCACTTCTATGCATACCTGTGAGGTAGTCCACAATTCTAAGGTAAGGACGAA
G S R V K I R M D T P S G V K D S I P A

GGATCAACTACTCTTCACAGCTTCTGATGAAATTCCATATAATGGAAATATATTATGATC
CCTAGTTGATGAGAAGTGTGGAAGGACTACTTTAAGGTATATTACCTTATATAAATACTAG
W I N Y S S G L P D E I P Y N G I Y Y D

CACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAGTCGCTGA
GTGGGCTTCTCCTCTCCATATAGAAGGTTGTGGGTGCCGGTTTCTTTGGTTTCAGCGACT
P P E E E R Y I F Q H P R P K K P K S L

GAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAACTCATACGTGA
 CTTATATACTTAGAGTATAACCTTACTCATCAGGCCTCGGATTTTAATTGAGTATGCACT
 R I Y E S H I G M S S P E P K I N S Y V

Xmn I

HinD III

ATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGCGGTGCAAATTA
 TAAAACTCTACTTCAAGAAGGAGCGTATTTTTTCGAACCCATGTTACGCCACGTTTAAT
 N F R D E V L P R I K K L G Y N A V Q I

TGGCTATTCAAGAGCATTCTTATTATGCTAGTTTTGGTTATCATGTCACAAATTTTTTTG
 ACCGATAAGTTCTCGTAAGAATAATACGATCAAAACCAATAGTACAGTGTTTAAAAAAC
 M A I Q E H S Y Y A S F G Y H V T N F F

CACCAAGCAGCCGTTTTGGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATG
 GTGGTTCGTGCGCAAAACCTTGCGGGCTGCTGGAATTCAGAACTAACTATTTTCGAGTAC
 A P S S R F G T P D D L K S L I D K A H

Nsi I

AGCTAGGAATTGTTGTTCTCATGGACATTGTTTCACAGCCATGCATCAAATAATACTTTAG
 TCGATCCTTAACAACAAGAGTACCTGTAACAAGTGTCGGTACGTAGTTTATTATGAAATC
 E L G I V V L M D I V H S H A S N N T L

Sac I

ATGGAAGTGAACATGTTTGACGGCACCAGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTT
 TACCTGACTTGTACAAACTGCCGTGGCTATCAACAATGAAAGTGAGACCTCGAGCACCAA
 D G L N M F D G T D S C Y F H S G A R G

ATCATTGGATGTGGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAGGTATC
 TAGTAACCTACACCCTAAGGGCGGAAAAATTGATACCTTTGACCTCCATGAATCCATAG
 Y F W M W D S R L F N Y G N W E V L R Y

TTCTCTCAAATGCGAGATGGTGGTGGATGAGTTCAAATTTGATGGATTTAGATTTGATG
 AAGAGAGTTTACGCTCTACACCAACCTACTCAAGTTTAACTACCTAAATCTAAACTAC
 L L S N A R W W L D E F K F D G F R F D

GTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACG
CACACTGTAGTTACTACATATGAGTGGTGCCTAATAGCCACCCTAAGTGACCCTTGATGC
G V T S M M Y T H H G L S V G F T G N Y

1500

Hinc II

AGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACG
TCCTTATGAAACCTGAGCGTTGACTACACCTACGACAACACATAGACTACGACCAGTTGC
E E Y F G L A T D V D A V V Y L M L V N

1560

ATCTTATTCATGGGCTTTTCCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGC
TAGAATAAGTACCCGAAAAGGTCTACGTTAATGGTAACCACTTCTACAATCGCCTTACG
D L I H G L F P D A I T I G E D V S G M

1620

CGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGG
GCTGTAAACATAAGGGCAAGTTCTACCCCAACAACCGAACTGATAGCCGACGTATACC
P T F C I P V Q D G G V G F D Y R L H M

1680

CAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTG
GTTAACGACTATTTACCTAACTCAACGAGTTCTTTGCCCTACTCCTAACCTCTCACCCAC
A I A D K W I E L L K K R D E D W R V G

1740

ATATTGTTTCATACACTGACAAATAGAAGATGGTCCGAAAAGTGTGTTTCATACGCTGAAA
TATAACAAGTATGTGACTGTTTATCTTCTACCAGCCTTTTCACACAAAGTATGCGACTTT
D I V H T L T N R R W S E K C V S Y A E

1800

GTCATGATCAAGCTCTAGTCGGTGATAAACTATAGCATTCTGGCTGATGGACAAGGATA
CAGTACTAGTTCGAGATCAGCCACTATTTTGATATCGTAAGACCGACTACCTGTTCTAT
S H D Q A L V G D K T I A F W L M D K D

1860

TGTATGATTTTATGGCTCTGGATAGACCGCCAACATCATTAATAGATCGTGGGAAGCAT
ACATACTAAAATACCGAGACCTATCTGGCGGTTGTAGTAATTATCTAGCACCCCTATCGTA
M Y D F M A L D R P P T S L I D R G I A

1920

Asp 718
Kpn I

TGCACAAGATGATTAGGCTTGTAACCTATGGGATTAGGAGGAGAAGGGTACCTAAATTTCA
ACGTGTTCTACTAATCCGAACATTGATACCCTAATCCTCCTCTTCCCATGGATTTAAAGT
L H K M I R L V T M G L G G E G Y L N F

1980

EcoR I

TGGGAAATGAATTTCGGCCACCCTGAGTGGATTGATTTCCCTAGGGCTGAACAACACCTCT
ACCTTTTACTTAAGCCGGTGGGACTCACCTAACTAAAGGGATCCCGACTTGTTGTGGAGA
M G N E F G H P E W I D F P R A E Q H L

2040

CTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTG
GACTACTGAGTCATTAAGGGCCTTTGGTTAAGTCAATACTATTTACGTCTGCCTCTAAAC
S D D S V I P G N Q F S Y D K C R R R F

2100

Ssp I

ACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGC
TGGACCCTCTACGTCTTATAAATTCTATGGCACCCAACGTTCTTAAACTGGCCCGATACG
D L G D A E Y L R Y R G L Q E F D R A M

2160

AGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCATATCACGAAAGG
TCATAGAACTTCTATTTTATACTCAAATACTGAAGTCTTGTGGTCAAGTATAGTGCTTTCC
Q Y L E D K Y E F M T S E H Q F I S R K

2220

ATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTC
TACTTCCTCTATCCTACTAACATAAACTTTTTCTTTTGATCAAAAACAGAAATTAAG
D E G D R M I V F E K G N L V F V F N F

2280

ACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGG
TGACCTGTTTTTTCGATAAGTCTGATAGCGTATCCGACGGACTTCGGACCTTTTATGTTCC
H W T K S Y S D Y R I G C L K P G K Y K

2340

TTGCCTTGGACTCAGATGATCCACTTTTTTGGTGGCTTCGGGAGAATTGATCATAATGCCG
AACGGAACCTGAGTCTACTAGGTGAAAAACCACCGAAGCCCTCTTAACTAGTATTACGGC
V A L D S D D P L F G G F G R I D H N A

2400

Ssp I

AATATTTACCTTTGAAGGATGGTATGATGATCGTCTCGTTCAATTATGGTGTATGCAC
TTATAAAGTGGAAACTTCTACCATACTACTAGCAGGAGCAAGTTAATACCACATACGTG
E Y F T F E G W Y D D R P R S I M V Y A

2460

Fig. 12 (con.)

29/31

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Fig. 13

